



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Alderson, Mark R.
Goodwin, Raymond G.
Smith, Craig A.
- (ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand And Human Receptor That Binds Thereto
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seese, Kathryn A.
(B) REGISTRATION NUMBER: 32,172
(C) REFERENCE/DOCKET NUMBER: 2801-WO
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
(B) CLONE: murine 4-1BB-L

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 53..979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: Invitine, L

AGCCTATAAA	GCACGGGCAC	TGGCGGGAGA	CGTGCCTGA	CCGACCGTGG	TA ATG	55
					Met	
					1	
GAC CAG CAC ACA CTT GAT GTG GAG GAT ACC GCG GAT GCC AGA CAT CCA						103
Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro						
5	10	15				
GCA GGT ACT TCG TGC CCC TCG GAT GCG GCG CTC CTC AGA GAT ACC GGG						151
Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly						
20	25	30				
CTC CTC GCG GAC GCT GCG CTC CTC TCA GAT ACT GTG CGC CCC ACA AAT						199
Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn						
35	40	45				
GCC GCG CTC CCC ACG GAT GCT GCC TAC CCT GCG GTT AAT GTT CGG GAT						247
Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp						
50	55	60	65			
CGC GAG GCC GCG TGG CCG CCT GCA CTG AAC TTC TGT TCC CGC CAC CCA						295
Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro						
70	75	80				
AAG CTC TAT GGC CTA GTC GCT TTG GTT TTG CTG CTT CTG ATC GCC GCC						343
Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala Ala						
85	90	95				
TGT GTT CCT ATC TTC ACC CGC ACC GAG CCT CGG CCA GCG CTC ACA ATC						391
Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile						
100	105	110				
ACC ACC TCG CCC AAC CTG GGT ACC CGA GAG AAT AAT GCA GAC CAG GTC						439
Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val						
115	120	125				
ACC CCT GTT TCC CAC ATT GGC TGC CCC AAC ACT ACA CAA CAG GGC TCT						487
Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser						
130	135	140	145			
CCT GTG TTC GCC AAG CTA CTG GCT AAA AAC CAA GCA TCG TTG TGC AAT						535
Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn						
150	155	160				
ACA ACT CTG AAC TGG CAC AGC CAA GAT GGA GCT GGG AGC TCA TAC CTA						583
Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu						
165	170	175				
TCT CAA GGT CTG AGG TAC GAA GAA GAC AAA AAG GAG TTG GTG GTA GAC						631
Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp						
180	185	190				

AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr 195 200 205	679
TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu 210 215 220 225	727
CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val 230 235 240	775
GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp 245 250 255	823
AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG Ser Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu 260 265 270	871
AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu 275 280 285	919
TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC Ser Tyr Pro Asn Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp 290 295 300 305	967
AAC CCA TGG GAA TGAGAACTAT CCTCTTG TGACTCCTAGTT GCTAAGTCCT Asn Pro Trp Glu	1019
CAAGCTGCTA TGTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGTCTT	1079
TAAC TGGACT TGGTATTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCACTAG	1139
ATAGCATTAG TAAACTGCTG GGCA GCTGCT AGATAAAAAAA AAATTTCTAA ATCAAAGTTT	1199
ATATTTATAT TAATATATAA AAATAAAATGT GTTTGTAAAT AAAAAAAA AAAAAA	1254

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: *multiple*

Met. Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
1 5 10 15

Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
20 25 30

Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
35 40 45

Asn	Ala	Ala	Leu	Pro	Thr	Asp	Ala	Ala	Tyr	Pro	Ala	Val	Asn	Val	Arg
50							55					60			
Asp	Arg	Glu	Ala	Ala	Trp	Pro	Pro	Ala	Leu	Asn	Phe	Cys	Ser	Arg	His
65					70				75				80		
Pro	Lys	Leu	Tyr	Gly	Leu	Val	Ala	Leu	Val	Leu	Leu	Leu	Ile	Ala	
				85					90				95		
Ala	Cys	Val	Pro	Ile	Phe	Thr	Arg	Thr	Glu	Pro	Arg	Pro	Ala	Leu	Thr
				100				105				110			
Ile	Thr	Thr	Ser	Pro	Asn	Leu	Gly	Thr	Arg	Glu	Asn	Asn	Ala	Asp	Gln
				115				120				125			
Val	Thr	Pro	Val	Ser	His	Ile	Gly	Cys	Pro	Asn	Thr	Thr	Gln	Gln	Gly
					130		135				140				
Ser	Pro	Val	Phe	Ala	Lys	Leu	Leu	Ala	Lys	Asn	Gln	Ala	Ser	Leu	Cys
					145		150			155		—	160		
Asn	Thr	Thr	Leu	Asn	Trp	His	Ser	Gln	Asp	Gly	Ala	Gly	Ser	Ser	Tyr
					165				170				175		
Leu	Ser	Gln	Gly	Leu	Arg	Tyr	Glu	Glu	Asp	Lys	Glu	Leu	Val	Val	
					180			185			190				
Asp	Ser	Pro	Gly	Leu	Tyr	Tyr	Val	Phe	Leu	Glu	Leu	Lys	Leu	Ser	Pro
					195			200			205				
Thr	Phe	Thr	Asn	Thr	Gly	His	Lys	Val	Gln	Gly	Trp	Val	Ser	Leu	Val
					210			215			220				
Leu	Gln	Ala	Lys	Pro	Gln	Val	Asp	Asp	Phe	Asp	Asn	Leu	Ala	Leu	Thr
					225		230			235			240		
Val	Glu	Leu	Phe	Pro	Cys	Ser	Met	Glu	Asn	Lys	Leu	Val	Asp	Arg	Ser
					245			250				255			
Trp	Ser	Gln	Leu	Leu	Leu	Leu	Lys	Ala	Gly	His	Arg	Leu	Ser	Val	Gly
					260			265			270				
Leu	Arg	Ala	Tyr	Leu	His	Gly	Ala	Gln	Asp	Ala	Tyr	Arg	Asp	Trp	Glu
					275			280			285				
Leu	Ser	Tyr	Pro	Asn	Thr	Thr	Ser	Phe	Gly	Leu	Phe	Leu	Val	Lys	Pro
					290			295			300				
Asp	Asn	Pro	Trp	Glu											
				305											

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: human 4-1BB-L(7A)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: human, L

GTC ATG GAA TAC GCC TCT GAC GCT TCA CTG GAC CCC GAA GCC CCG TGG Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp 1 5 10 15	48
CCT CCC GCG CCC CGC GCT CGC GCC TGC CGC GTA CTG CCT TGG GCC CTG Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu 20 25 30	96
GTC GCG GGG CTG CTG CTG CTG CTC GCT GCC GCC TGC GCC GTC Val Ala Gly Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val 35 40 45	144
TTC CTC GCC TGC CCC TGG GCC GTG TCC GGG GCT CGC GCC TCG CCC GGC Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly 50 55 60	192
TCC GCG GCC AGC CCG AGA CTC CGC GAG GGT CCC GAG CTT TCG CCC GAC Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp 65 70 75	240
GAT CCC GCC GGC CTC TTG GAC CTG CGG CAG GGC ATG TTT GCG CAG CTG Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu 80 85 90 95	288
GTG GCC CAA AAT GTT CTG CTG ATC GAT GGG CCC CTG AGC TGG TAC AGT Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser 100 105 110	336
GAC CCA GGC CTG GCA GGC GTG TCC CTG ACG GGG GGC CTG AGC TAC AAA Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Leu Ser Tyr Lys 115 120 125	384
GAG GAC ACG AAG GAG CTG GTG GTG GCC AAG GCT GGA GTC TAC TAT GTC Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val 130 135 140	432
TTC TTT CAA CTA GAG CTG CGG CGC GTG GTG GCC GGC GAG GGC TCA GGC Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly 145 150 155	480
TCC GTT TCA CTT GCG CTG CAC CTG CAG CCA CTG CGC TCT GCT GCT GGG Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly 160 165 170 175	528

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: *human L*

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
100 105 110

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
115 120 125

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
245 250

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 768 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: mu4-1BB

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..768

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 70..768

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: *W K L Y V A L I*

ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Val	48
-23 -20 -15 -10	
GGC TGT GAG AAG GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TGT CAG Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln	96
-5 1 5	
CCT GGT ACT TTC TGC AGA AAA TAC AAT CCA GTC TGC AAG AGC TGC CCT Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro	144
10 15 20 25	
CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC TGT AAC ATC TGC Pro Ser Thr Phe Ser Ser Ile Gly Gln Pro Asn Cys Asn Ile Cys	192
30 35 40	
AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr	240
45 50 55	
CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro	288
60 65 70	
CAG TGC ACC AGA TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr	336
75 80 85	
AAG CAG GGT TGC AAA ACC TGT AGC TTG GGA ACA TTT AAT GAC CAG AAC Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn	384
90 95 100 105	
GGT ACT GGC GTC TGT CGA CCC TGG ACG AAC TGC TCT CTA GAC GGA AGG Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg	432
110 115 120	

TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC	480
Ser Val Leu Lys Thr Gly Thr Glu Lys Asp Val Val Cys Gly Pro	
125 130 135	
CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG	528
Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu	
140 145 150	
GGA GGA CCA GGA GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG	576
Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala	
155 160 165	
CTG ACA TCG GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC	624
Leu Thr Ser Ala Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe	
170 175 180 185	
TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC ATA TTC AAG CAA	672
Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln	
190 195 200	
CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC	720
Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser	
205 210 215	
TGC CGA TGT CCA CAG GAA GAA GGA GGA GGA GGA GGC TAT GAG CTG	768
Cys Arg Cys Pro Gln Glu Glu Gly Gly Gly Gly Tyr Glu Leu	
220 225 230	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
 -23 -20 -15 . -10

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
-5 1 5

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
10 15 20 25

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
45 50 55

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
60 65 70

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
75 80 85

Lys	Gln	Gly	Cys	Lys	Thr	Cys	Ser	Leu	Gly	Thr	Phe	Asn	Asp	Gln	Asn
90											100			105	
Gly	Thr	Gly	Val	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Arg
			110						115					120	
Ser	Val	Leu	Lys	Thr	Gly	Thr	Glu	Lys	Asp	Val	Val	Cys	Gly	Pro	
			125				130					135			
Pro	Val	Val	Ser	Phe	Ser	Pro	Ser	Thr	Thr	Ile	Ser	Val	Thr	Pro	Glu
								145					150		
Gly	Gly	Pro	Gly	Gly	His	Ser	Leu	Gln	Val	Leu	Thr	Leu	Phe	Leu	Ala
					155			160			165				
Leu	Thr	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Ile	Phe	Ile	Thr	Leu	Leu	Phe
						175				180					185
Ser	Val	Leu	Lys	Trp	Ile	Arg	Lys	Lys	Phe	Pro	His	Ile	Phe	Lys	Gln
					190				195				—	200	
Pro	Phe	Lys	Lys	Thr	Thr	Gly	Ala	Ala	Gln	Glu	Glu	Asp	Ala	Cys	Ser
					205				210				215		
Cys	Arg	Cys	Pro	Gln	Glu	Glu	Gly	Gly	Gly	Gly	Tyr	Glu	Leu		
					220			225			230				

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: hu4-1BB
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 120..887
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 189..884
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 120..188

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 7:

AGTGGAAAGT TCTCCGGCAG CCCTGAGATC TCAAGAGTGA CATTGTGAG ACCAGCTAAT	60
TTGATTAAAA TTCTCTTGGG ATCAGCTTG CTAGTATCAT ACCTGTGCCA GATTCATC	119
ATG GGA AAC AGC TGT TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu	167
-23 -20 -15 -10	
AAC TTT GAG AGG ACA AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro	215
-5 1 5	
GCT GGT ACA TTC TGT GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT Ala Gly Thr Phe Cys Asp Asn Arg Asn Gln Ile Cys Ser Pro Cys	263
10 15 20 25	
CCT CCA AAT AGT TTC TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile	311
30 35 40	
TGC AGG CAG TGT AAA GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser	359
45 50 55	
ACC AGC AAT GCA GAG TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly	407
60 65 70	
GCA GGA TGC AGC ATG TGT GAA CAG GAT TGT AAA CAA GGT CAA GAA CTG Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu	455
75 80 85	
ACA AAA AAA GGT TGT AAA GAC TGT TGC TTT GGG ACA TTT AAC GAT CAG Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln	503
90 95 100 105	
AAA CGT GGC ATC TGT CGA CCC TGG ACA AAC TGT TCT TTG GAT GGA AAG Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys	551
110 115 120	
TCT GTG CTT GTG AAT GGG ACG AAG GAG AGG GAC GTG GTC TGT GGA CCA Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro	599
125 130 135	
TCT CCA GCC GAC CTC TCT CCG GGA GCA TCC TCT GTG ACC CCG CCT GCC Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala	647
140 145 150	
CCT GCG AGA GAG CCA GGA CAC TCT CCG CAG ATC ATC TCC TTC TTT CTT Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu	695
155 160 165	
GCG CTG ACG TCG ACT GCG TTG CTC TTC CTG CTG TTC CTC CTC ACG CTC Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu	743
170 175 180 185	

CGT TTC TCT GTT AAA CGG GGC AGA AAG AAA CTC CTG TAT ATA TTC	791
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe	
190 195 200	
AAA CAA CCA TTT ATG AGA CCA GTA CAA ACT ACT CAA GAG GAA GAT GGC	839
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly	
205 210 215	
TGT AGC TGC CGA TTT CCA GAA GAA GAA GGA GGA TGT GAA CTG TGAAATGGAA	
894	
Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu	
220 225 230	
GTCAATAGGG CTGTTGGAC TTTCTTGAAA AGAACAGG AAATATGAGT CATCCGCTAT	954
CACAGCTTTC AAAAGCAAGA ACACCACCT ACATAATACC CAGGATTCCC CCAACACACG	1014
TTCTTTCTA AATGCCAATG AGTTGGCCTT TAAAAATGCA CCACCTTTTT TTTTTTTTT	1074
GACAGGGTCT CACTCTGTCA CCCAGGCTGG AGTGCAGTGG CACCACCATG GCTCTTGCA	1134
GCCTTGACCT CTGGGAGCTC AAGTGATCCT CCTGCCTCAG TCTCCTAGTA GCTGGAACTA	1194
CAAGGAAGGG CCACCACACC TGACTAACTT TTTTGTTTTT TGTTGGTAA AGATGGCATT	1254
TCGCCATGTT GTACAGGCTG GTCTCAAACCT CCTAGGTTCA CTTTGGCCTC CCAAAGTGCT	1314
GGGATTACAG ACATGAACTG CCAGGCCCGG CCAAAATAAT GCACCACTTT TAACAGAACAA	1374
GACAGATGAG GACAGAGCTG GTGATAAAAAA AAAAAAAAAA A	1415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: Human, R

Met	Gly	Asn	Ser	Cys	Tyr	Asn	Ile	Val	Ala	Thr	Leu	Leu	Leu	Val	Leu
-23							-20				-15			-10	

Asn	Phe	Glu	Arg	Thr	Arg	Ser	Leu	Gln	Asp	Pro	Cys	Ser	Asn	Cys	Pro
							-5				1		5		

Ala	Gly	Thr	Phe	Cys	Asp	Asn	Asn	Arg	Asn	Gln	Ile	Cys	Ser	Pro	Cys
10							15			20			25		

Pro	Pro	Asn	Ser	Phe	Ser	Ser	Ala	Gly	Gly	Gln	Arg	Thr	Cys	Asp	Ile
							30			35			40		

Cys	Arg	Gln	Cys	Lys	Gly	Val	Phe	Arg	Thr	Arg	Lys	Glu	Cys	Ser	Ser
							45			50			55		

Thr	Ser	Asn	Ala	Glu	Cys	Asp	Cys	Thr	Pro	Gly	Phe	His	Cys	Leu	Gly
							60			65			70		

AL

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu →
 75 80 85
 Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln →
 90 95 100 105
 Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys →
 110 115 120
 Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro →
 125 130 135
 Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala →
 140 145 150
 Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu →
 155 160 165
 Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu →
 170 175 180 185
 Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe →
 190 195 200
 Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly →
 205 210 215
 Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu →
 220 225 230

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCACTAGTT CTGTGCAGAA CTCCTGTGAT AAC
33

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: *11, 1/1, continue*

CACAAGATCT GGGCTCCTCT GGAGTCACAG AAATG
35

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: *12, 1/1, continue*

CAGACTAGTT CACTCTGGAG TCACAGAAAT G
31

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: *13, 1/1, continue*

ATAGCGGCCG CTGCCAGATT TCATCATGGG AAAC.
34

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: *14, 1/1, continue*

ACAAGATCTG GGCTCCTGCG GAGAGTGTCC TGGCTCTCTC
40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: hIgG1Fc
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: *Tat 1*

G	GTA	CCG	CTA	GCG	TCG	ACA	GGC	CTA	GGA	TAT	CGA	TAC	GTA	GAG	CCC	46
Val	Pro	Leu	Ala	Ser	Thr	Gly	Leu	Gly	Tyr	Arg	Tyr	Val	Glu	Pro		
1															15	
AGA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	94
Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
															30	
20																
CTC	CTG	GGG	GGG	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	142
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
															45	
35																
ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	190
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
															50	
50															60	
GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	238
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
															65	
65															75	
GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	CAG	TAC	AAC	286	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
															80	
80															90	
AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	334
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
															100	
100															105	
CTG	AAT	GGC	AAG	GAC	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	382
Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	
															115	
115															120	
GCC	CCC	ATG	CAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	430
Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
															130	
130															135	
															140	
															140	

CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn 145 150 155	478
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile 160 165 170 175	526
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 180 185 190	574
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 195 200 205	622
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 210 215 220	670
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 225 230 235	718
TCC CTG TCT CCG GGT AAA TGAACCTAGT Ser Leu Ser Pro Gly Lys 240 245	745

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Pro Leu Ala Ser Thr Gly Leu Gly Tyr Arg Tyr Val Glu Pro Arg
1 5 10 15.

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
20 25 30

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
35 40 45

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
50 55 60

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
65 70 75 80

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
85 90 95

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
100 105 110

Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
115 120 125

Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
130 135 140

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
145 150 155 160

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala
165 170 175

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
180 185 190

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
195 200 205

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
210 215 220

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
225 230 235 240

Leu Ser Pro Gly Lys
245